

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/821,231A

Source:

FEED

Date Processed by STIC:

2-4-05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/821,231A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ **Wrapped Nucleics**  
**Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2        **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3        **Misaligned Amino Numbering** The numbering under each 3<sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4        **Non-ASCII** The submitted file was not saved in ASCII(DOS)ical, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5        **Variable Length** Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6        **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7        **Skipped Sequences (OLD RULES)** Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(x) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8        **Skipped Sequences (NEW RULES)** Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9        **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10        **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown, or is Artificial Sequence.

11        **Use of <220>** Sequence(s)        missing the <220>-<223> "feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12        **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13        **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 02/04/2005

PATENT APPLICATION: US/10/821,231A

TIME: 15:27:18

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\02042005\J821231A.raw

1 <110> APPLICANT: Dongmao Zhang  
 3 <120> TITLE OF INVENTION: Process and Apparatus for Segregation and Testing by  
 Spectral Analysis of  
 4 Solid Deposits Derived From Liquid Mixtures  
 6 <130> FILE REFERENCE: 12264/017  
 8 <140> CURRENT APPLICATION NUMBER: 10/821231A  
 9 <141> CURRENT FILING DATE: 2004-04-08  
 11 <150> PRIOR APPLICATION NUMBER: us 60/462083  
 12 <151> PRIOR FILING DATE: 2003-04-11  
 14 <150> PRIOR APPLICATION NUMBER: us 60/462472  
 15 <151> PRIOR FILING DATE: 2003-04-11  
 17 <150> PRIOR APPLICATION NUMBER: us 60/490057  
 18 <151> PRIOR FILING DATE: 2003-07-25  
 20 <150> PRIOR APPLICATION NUMBER: us 60/554701  
 21 <151> PRIOR FILING DATE: 2004-03-19  
 23 <150> PRIOR APPLICATION NUMBER: us 60/551311  
 24 <151> PRIOR FILING DATE: 2004-03-08  
 26 <160> NUMBER OF SEQ ID NOS: 1  
 28 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply  
 Corrected Diskette Needed

(ps.1)

## ERRORED SEQUENCES

30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 536  
 32 <212> TYPE: PRT  
 33 <213> ORGANISM: Homo sapiens  
 35 <400> SEQUENCE: 1  
 37 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
 E--> 38 1 5 10  
 E--> 39 15  
 42 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
 E--> 43 20 25  
 E--> 44 30  
 47 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
 E--> 48 35 40  
 51 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
 E--> 52 50 55 60  
 55 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 E--> 56 65 70 75  
 E--> 57 80  
 60 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 E--> 61 85 90  
 E--> 62 95

-P/S see  
 item #  
 on  
 error  
 summary  
 sheet.

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TIME: 15:27:18

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\02042005\J821231A.raw

```

65 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
E--> 66                      100                      105
E--> 67 110
70 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
E--> 71                      115                      120
74 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
E--> 75                      130                      135                      140
78 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
E--> 79 145                      150                      155
E--> 80 160
83 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
E--> 84                      165                      170
E--> 85 175
88 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
E--> 89                      180                      185
E--> 90 190
93 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
E--> 94                      195                      200
E--> 97 Lvs Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
E--> 98                      210                      215                      220
101 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
E--> 102 225                      230                      235
E--> 103 240
106 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
E--> 107                      245                      250
E--> 108 255
111 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
E--> 112                      260                      265
E--> 113 270
116 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
E--> 117                      275                      280                      285
120 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
E--> 121                      290                      295                      300
124 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
E--> 125 305                      310                      315
E--> 126 320
129 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
E--> 130                      325                      330
E--> 131 335
134 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
E--> 135                      340                      345                      350
138 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
E--> 139                      355                      360                      365
142 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
E--> 143                      370                      375                      380
146 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
E--> 147 385                      390                      395
E--> 148 400
151 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp

```

125 — PLS  
See  
item #  
1 on  
error  
Summary  
Sheet.

DATE: 02/04/2005

TIME: 15:27:18

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\02042005\J821231A.raw

```

E--> 152
E--> 153 415
156 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
E--> 157 420 425 430
160 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
E--> 161 435 440 445
164 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
E--> 165 450 455 460
168 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
E--> 169 465 470 475
E--> 170 480
173 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
E--> 174 485 490
E--> 175 495
178 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
E--> 179 500 505
E--> 180 510
183 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
E--> 184 515 520 525
187 Gln Tyr Gln Pro Gly Glu Asn Leu
E--> 188 530 535

```

See item  
# 1 on  
error  
summary  
sheet.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/821,231A

DATE: 02/04/2005  
TIME: 15:27:19

Input Set : A:\PTO.FG.txt  
Output Set: N:\CRF4\02042005\J821231A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3,38,43,48,52,56,61,66,71,75,79,84,94,98,102,107,117,121

Seq#:1; Line(s) 125,130,135,139,143,147,152,157,161,165,169,174,179,184

VERIFICATION SUMMARY

DATE: 02/04/2005

PATENT APPLICATION: US/10/821,231A

TIME: 15:27:19

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\02042005\J821231A.raw

L:38 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1

M:332 Repeated in SeqNo=1

L:97 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1